

OIKE

## RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/966,147

TIME: 14:24:21

Input Set : A:\GENENT.33CPC4Cseqlist.txt

Output Set: N:\CRF3\11072001\I966147.raw

## SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Presta, Leonard G.

6 Shelton, David L.

7 Urfer, Roman

9 (ii) TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS

11 (iii) NUMBER OF SEQUENCES: 41

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP

15 (B) STREET: 620 Newport Center Drive, 16th Floor

16 (C) CITY: Newport Beach

17 (D) STATE: California

18 (E) COUNTRY: USA

19 (F) ZIP: 92660

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: WinPatin (Genentech)

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/966,147 *OK*

C--> 29 (B) FILING DATE: 27-Sep-2000 *OK*

30 (C) CLASSIFICATION:

C--> 40 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/446172

34 (B) FILING DATE: 19-MAY-1995

37 (A) APPLICATION NUMBER: 08/286846

38 (B) FILING DATE: 05-AUG-1994

41 (A) APPLICATION NUMBER: 08/215139

42 (B) FILING DATE: 18-MAR-1994

C--> 44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Dreger, Ginger

46 (B) REGISTRATION NUMBER: 33,055

47 (C) REFERENCE/DOCKET NUMBER: GENENT.33CPC4C

C--> 49 (ix) TELECOMMUNICATION INFORMATION: *OK*

50 (A) TELEPHONE: (415) 954-4114

51 (B) TELEFAX: (415) 954-4111

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 3194 base pairs

57 (B) TYPE: Nucleic Acid

58 (C) STRANDEDNESS: Single

59 (D) TOPOLOGY: Linear *OK*

W--> 60 (ii) MOLECULE TYPE: nucleic acid

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65 GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50

67 GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

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```

69 CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
71 CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
73 TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
75 CGACCCCTTCT CCTGGCATCG TGGCATTTCG GAGATTGGAG CCTAACAGTG 300
77 TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
79 GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400
81 GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
83 AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
85 TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
87 GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
89 AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
91 AGCAGCAAGA ATATCCCTCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
93 GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
95 CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
97 TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
99 ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGAAGC 900
101 AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950
103 AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
105 CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCTCAAC 1050
107 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
109 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
111 CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
113 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
115 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
117 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
119 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
121 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
123 CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500
125 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
127 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600
129 TGGCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
131 ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700
133 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750
135 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800
137 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
139 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
141 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950
143 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000
145 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCAC 2050
147 GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCAGCAG ATCGCCGCGG 2100
149 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150
151 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200
153 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
155 CAATGCTGCC CATTGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300
157 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
159 TTTACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400
161 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450
163 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500
165 GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550

```

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```

167 CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
169 GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650
171 AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700
173 ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750
175 TCCATAGACA CAGTATTGAC TTCTTTTTGG CATTATCTCT TTCTCTCTTT 2800
177 CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTTCTTC 2850
179 TTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCTTTC TTTTGAATCA 2900
181 ATCTGGCTTC TGCATTACTA TTAACCTCTGC ATAGACAAAG GCCTTAACAA 2950
183 ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCAC CACAATAAC 3000
185 AATGCCTTGT TGTATTCTCG CCTTTGATGT GGATGAAAAA AAGGGAAAAC 3050
187 AAATATTTCA CTTAAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100
189 TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150
191 TTGGATGGCT TAAGCCTGTG TATAAAAAAA AAAAAAATC TAGA 3194

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193 (2) INFORMATION FOR SEQ ID NO: 2:

195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 822 amino acids

197 (B) TYPE: Amino Acid

198 (D) TOPOLOGY: Linear

200 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

202 Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu
203 1 5 10 15
205 Trp Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe
206 20 25 30
208 Ala Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys
209 35 40 45
211 Ser Asp Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro
212 50 55 60
214 Asn Ser Val Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn
215 65 70 75
217 Gln Lys Arg Leu Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr
218 80 85 90
220 Val Gly Leu Arg Asn Leu Thr Ile Val Asp Ser Gly Leu Lys Phe
221 95 100 105
223 Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile
224 110 115 120
226 Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe
227 125 130 135
229 Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe
230 140 145 150
232 Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala
233 155 160 165
235 Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser
236 170 175 180
238 Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly
239 185 190 195
241 Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu
242 200 205 210
244 Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val
245 215 220 225

```

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247	Pro	Asn	Met	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His	Met
248					230					235					240
250	Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile
251					245					250					255
253	Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn
254					260					265					270
256	Leu	Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe
257					275					280					285
259	Ala	Pro	Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His
260					290					295					300
262	Trp	Cys	Ile	Pro	Phe	Thr	Val	Lys	Gly	Asn	Pro	Lys	Pro	Ala	Leu
263					305					310					315
265	Gln	Trp	Phe	Tyr	Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile
266					320					325					330
268	Cys	Thr	Lys	Ile	His	Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys
269					335					340					345
271	Leu	Gln	Leu	Asp	Asn	Pro	Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr
272					350					355					360
274	Leu	Ile	Ala	Lys	Asn	Glu	Tyr	Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser
275					365					370					375
277	Ala	His	Phe	Met	Gly	Trp	Pro	Gly	Ile	Asp	Asp	Gly	Ala	Asn	Pro
278					380					385					390
280	Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp	Tyr	Gly	Thr	Ala	Ala	Asn
281					395					400					405
283	Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn	Glu	Ile	Pro	Ser	Thr
284					410					415					420
286	Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Leu	Ser	Val	Tyr	Ala
287					425					430					435
289	Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu	Leu	Val	Met
290					440					445					450
292	Leu	Phe	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly	Met	Lys
293					455					460					465
295	Gly	Pro	Ala	Ser	Val	Ile	Ser	Asn	Asp	Asp	Asp	Ser	Ala	Ser	Pro
296					470					475					480
298	Leu	His	His	Ile	Ser	Asn	Gly	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Glu
299					485					490					495
301	Gly	Gly	Pro	Asp	Ala	Val	Ile	Ile	Gly	Met	Thr	Lys	Ile	Pro	Val
302					500					505					510
304	Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Gly	Ile	Thr	Asn	Ser	Gln	Leu	Lys
305					515					520					525
307	Pro	Asp	Thr	Phe	Val	Gln	His	Ile	Lys	Arg	His	Asn	Ile	Val	Leu
308					530					535					540
310	Lys	Arg	Glu	Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala
311					545					550					555
313	Glu	Cys	Tyr	Asn	Leu	Cys	Pro	Glu	Gln	Asp	Lys	Ile	Leu	Val	Ala
314					560					565					570
316	Val	Lys	Thr	Leu	Lys	Asp	Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe
317					575					580					585
319	His	Arg	Glu	Ala	Glu	Leu	Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile

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320		590		595		600
322	Val Lys Phe Tyr Gly	Val Cys Val Glu Gly	Asp Pro Leu Ile Met			
323		605		610		615
325	Val Phe Glu Tyr Met	Lys His Gly Asp	Leu Asn Lys Phe Leu Arg			
326		620		625		630
328	Ala His Gly Pro Asp	Ala Val Leu Met	Ala Glu Gly Asn Pro Pro			
329		635		640		645
331	Thr Glu Leu Thr Gln	Ser Gln Met Leu	His Ile Ala Gln Gln Ile			
332		650		655		660
334	Ala Ala Gly Met Val	Tyr Leu Ala Ser	Gln His Phe Val His Arg			
335		665		670		675
337	Asp Leu Ala Thr Arg	Asn Cys Leu Val	Gly Glu Asn Leu Leu Val			
338		680		685		690
340	Lys Ile Gly Asp Phe	Gly Met Ser Arg	Asp Val Tyr Ser Thr Asp			
341		695		700		705
343	Tyr Tyr Arg Val Gly	Gly His Thr Met	Leu Pro Ile Arg Trp Met			
344		710		715		720
346	Pro Pro Glu Ser Ile	Met Tyr Arg Lys	Phe Thr Thr Glu Ser Asp			
347		725		730		735
349	Val Trp Ser Leu Gly	Val Val Leu Trp	Glu Ile Phe Thr Tyr Gly			
350		740		745		750
352	Lys Gln Pro Trp Tyr	Gln Leu Ser Asn	Asn Glu Val Ile Glu Cys			
353		755		760		765
355	Ile Thr Gln Gly Arg	Val Leu Gln Arg	Pro Arg Thr Cys Pro Gln			
356		770		775		780
358	Glu Val Tyr Glu Leu	Met Leu Gly Cys	Trp Gln Arg Glu Pro His			
359		785		790		795
361	Met Arg Lys Asn Ile	Lys Gly Ile His	Thr Leu Leu Gln Asn Leu			
362		800		805		810
364	Ala Lys Ala Ser Pro	Val Tyr Leu Asp	Ile Leu Gly			
365		815		820		

367 (2) INFORMATION FOR SEQ ID NO: 3:

369 (i) SEQUENCE CHARACTERISTICS:

370 (A) LENGTH: 1870 base pairs

371 (B) TYPE: Nucleic Acid

372 (C) STRANDEDNESS: Single

373 (D) TOPOLOGY: Linear

375 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

378	GGAAGGTTTA	AAGAAGAAGC	CGCAAAGCGC	AGGGAAGGCC	TCCCGGCACG	50
380	GGTGGGGGAA	AGCGGCCGGT	GCAGCGCGGG	GACAGGCACT	CGGGCTGGCA	100
382	CTGGCTGCTA	GGGATGTCGT	CCTGGATAAG	GTGGCATGGA	CCCGCCATGG	150
384	CGCGGCTCTG	GGGCTTCTGC	TGGCTGGTTG	TGGGCTTCTG	GAGGGCCGCT	200
386	TTCGCCTGTC	CCACGTCCTG	CAAATGCAGT	GCCTCTCGGA	TCTGGTGCAG	250
388	CGACCCTTCT	CCTGGCATCG	TGGCATTTCC	GAGATTGGAG	CCTAACAGTG	300
390	TAGATCCTGA	GAACATCACC	GAAATTTTCA	TCGCAAACCA	GAAAAGGTTA	350
392	GAAATCATCA	ACGAAGATGA	TGTTGAAGCT	TATGTGGGAC	TGAGAAATCT	400
394	GACAATTGTG	GATTCTGGAT	TAAATTTTGT	GGCTCATAAA	GCATTTCTGA	450
396	AAAACAGCAA	CCTGCAGCAC	ATCAATTTTA	CCCGAAACAA	ACTGACGAGT	500
398	TTGTCTAGGA	AACATTTCCG	TCACCTTGAC	TTGTCTGAAC	TGATCCTGGT	550

## VERIFICATION SUMMARY

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Input Set : A:\GENENT.33CPC4Cseqlist.txt

Output Set: N:\CRF3\11072001\I966147.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:40 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:44 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
L:49 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]  
L:60 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1